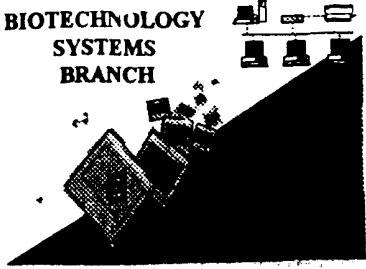Strzelecka

#11

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/530,746_

Source: _1656_

Date Processed by STIC: _4/30/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION   SERIAL NUMBER: _C9/53C, 746_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>**
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES)   **<210> sequence id number**
<400> sequence id number
000

10 _____ Use of **n's** or **Xaa's**   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 _____ Use of "Artificial"   Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES)   Valid response is Artificial Sequence.

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing)
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1656

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,746

DATE: 04/30/2001
TIME: 17:59:38

[handwritten: pp 1-4]

*[handwritten: Does Not Comply
Correcto Diskette Needed]*

Input Set : A:\4817 0Q.txt
Output Set: N:\CRF3\04302001\I530746.raw

3 <110> APPLICANT: Kessler, Christoph
4   Haberhausen, Gerd
5   Bartl, Knut
6   Orum, Henrik
8 <120> TITLE OF INVENTION: SPECIFIC AND SENSITIVE NUCLEIC ACID DETECTION METHOD
11 <130> FILE REFERENCE: 4817/OQ
13 **<140> CURRENT APPLICATION NUMBER: US/09/530,746**
14 **<141> CURRENT FILING DATE: 2000-11-16**
16 <160> NUMBER OF SEQ ID NOS: 94
18 <170> SOFTWARE: PatentIn Version 3.0

ERRORED SEQUENCES

248 <210> SEQ ID NO: 21
249 <211> LENGTH: 11
250 <212> TYPE: DNA   *[handwritten: see item 11 (on 2nd summary sheet)]*
C--> 251 <213> ORGANISM: Artificial
253 <220> FEATURE:
254 <223> OTHER INFORMATION: amplification primer
256 <400> SEQUENCE: 21
E--> 257 cgtactgcct (iatagggtic t   *[handwritten: do not show "i" in the sequence itself. Use "n" and explain in <220>-<225> section (Per sequence rules)]*   21
260 <210> SEQ ID NO: 22
261 <211> LENGTH: 23
262 <212> TYPE: DNA   *[handwritten: item 11]*
C--> 263 <213> ORGANISM: Artificial
265 <220> FEATURE:
266 <223> OTHER INFORMATION: amplification primer
268 <400> SEQUENCE: 22
E--> 269 gmatgtgmta mggtmtdmid gdc   *[handwritten: invalid - use N and explain]*   23
272 <210> SEQ ID NO: 23
273 <211> LENGTH: 20
274 <212> TYPE: DNA
C--> 275 <213> ORGANISM: Artificial   *[handwritten: item 11]*
277 <220> FEATURE:
278 <223> OTHER INFORMATION: amplification primer
280 <400> SEQUENCE: 23
E--> 281 cgtactgcct (iatagggtic   *[handwritten: invalid]*   20
284 <210> SEQ ID NO: 24
285 <211> LENGTH: 21
286 <212> TYPE: DNA
C--> 287 <213> ORGANISM: Artificial   *[handwritten: item 11]*
289 <220> FEATURE:
290 <223> OTHER INFORMATION: amplification primer
292 <400> SEQUENCE: 24
E--> 293 cgtamtgmmt (iatagggtim t   *[handwritten: invalid]*   21
296 <210> SEQ ID NO: 25

RAW SEQUENCE LISTING   DATE: 04/30/2001
PATENT APPLICATION: US/09/530,746   TIME: 17:59:38

Input Set : A:\4817 0Q.txt
Output Set: N:\CRF3\04302001\I530746.raw

```
           297 <211> LENGTH: 23
           298 <212> TYPE: DNA
C--> 299 <213> ORGANISM: Artificial      item 11
           301 <220> FEATURE:
           302 <223> OTHER INFORMATION: amplification primer
           304 <400> SEQUENCE  25       invalid - use "n" and explain
E--> 305 gmatgpppa mggtmtdmid gdm                                  23
           308 <210> SEQ ID NO: 16
           309 <211> LENGTH: 20
           310 <212> TYPE: DNA
C--> 311 <213> ORGANISM: Artificial      item 11
           313 <220> FEATURE:
           314 <223> OTHER INFORMATION: amplification primer
           316 <400> SEQUENCE  26       invalid
E--> 317 cgtamtgmmt iataggggtim                                    20
           332 <210> SEQ ID NO: 28
           333 <211> LENGTH: 21
           334 <212> TYPE  DNA
C--> 335 <213> ORGANISM: Artificial
           337 <220> FEATURE:
           338 <223> OTHER INFORMATION: amplification primer
           340 <400> SEQUENCE: 28       invalid
E--> 341 cgtamtgmmt iatagggtic t                                   21
           344 <210> SEQ ID NO: 29
           345 <211> LENGTH: 26
           346 <212> TYPE: DNA
C--> 347 <213> ORGANISM: Artificial
           349 <220> FEATURE:
           350 <223> OTHER INFORMATION: amplification primer
           352 <400> SEQUENCE  29       invalid
E--> 353 gmatgtgmta mggtmtdmid gdmttc                              26
           356 <210> SEQ ID NO: 30
           357 <211> LENGTH: 20
           358 <212> TYPE: DNA
C--> 359 <213> ORGANISM: Artificial
           361 <220> FEATURE:
           362 <223> OTHER INFORMATION: amplification primer
           364 <400> SEQUENCE: 30       invalid
E--> 365 cgtamtgmmt iatagggtic                                     20
           368 <210> SEQ ID NO  31
           369 <211> LENGTH: 26
           370 <212> TYPE: DNA
C--> 371 <213> ORGANISM: Artificial
           373 <220> FEATURE:
           374 <223> OTHER INFORMATION: amplification primer
           376 <400> SEQUENCE: 31       invalid
E--> 377 gmatgtgmta mggtmtdmid gdmptc                              26
           380 <210> SEQ ID NO: 32
           381 <211> LENGTH: 26
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,746

Input Set : A:\4817 0Q.txt
Output Set: N:\CRF3\04302001\I530746.raw

```
         TYPE: DNA
C--> 383 <213> ORGANISM: Artificial
         FEATURE
         OTHER INFORMATION: amplification primer
         <400> SEQUENCE 32
E--> 389 gmatgpkppa mggtmtdmid gdmptm                              26
     416 <210> SEQ ID NO: 35
     417 <211> LENGTH: 18
     418 <212> TYPE: DNA
C--> 419 <213> ORGANISM: Artificial
     421 <220> FEATURE:
     422 <223> OTHER INFORMATION: amplification primer
     424 <400> SEQUENCE 35
E--> 425 cgtamtgmmt iataggggt                                      18
     428 <210> SEQ ID NO: 36
     429 <211> LENGTH: 17
     433 <212> TYPE: DNA
C--> 431 <213> ORGANISM: Artificial
     433 <220> FEATURE:
     434 <223> OTHER INFORMATION: amplification primer
     436 <400> SEQUENCE 36
E--> 437 gmatgtgmta mgitmtamia gamttmc                             27
     440 <210> SEQ ID NO: 37
     441 <211> LENGTH: 17
     442 <212> TYPE: DNA
C--> 443 <213> ORGANISM: Artificial
     445 <220> FEATURE:
     446 <223> OTHER INFORMATION  amplification primer
     448 <400> SEQUENCE  37
E--> 449 gmatgtgmta mggtmtamia gamptmc                             27
     452 <210> SEQ ID NO  38
     453 <211> LENGTH: 17
     454 <212> TYPE  DNA
C--> 455 <213> ORGANISM  Artificial
     457 <220> FEATURE.
     458 <223> OTHER INFORMATION: amplification primer
     460 <400> SEQUENCE  38
E--> 461 gmatgtgmta mggtmtamia gamptmm                             27
     464 <210> SEQ ID NO  39
     465 <211> LENGTH: 18
     466 <212> TYPE  DNA
C--> 467 <213> ORGANISM: Artificial
     469 <220> FEATURE:
     470 <223> OTHER INFORMATION: amplification primer
     472 <400> SEQUENCE  39
E--> 473 cgtdmtgmmt idtdgggt                                       18
     476 <210> SEQ ID NO  40
     477 <211> LENGTH: 17
     478 <212> TYPE: DNA
```

file: C: CRF3 Outhold VsrI530746.htm   4 30 01

RAW SEQUENCE LISTING   DATE: 04/30/2001
PATENT APPLICATION: US/09/530,746   TIME: 17:59:38

Input Set : A:\4817 0Q.txt
Output Set: N:\CRF3\04302001\I530746.raw

C--> 479 <213> ORGANISM: Artificial
     481 <220> FEATURE:
     482 <223> OTHER INFORMATION: amplification primer
     484 <400> SEQUENCE: 40
E--> 485 gmatgpkppa mgitmtamia gamptmc   ) invalid   27
     488 <210> SEQ ID NO: 41
     489 <211> LENGTH: 27
     490 <212> TYPE: DNA
C--> 491 <213> ORGANISM: Artificial
     493 <220> FEATURE:
     494 <223> OTHER INFORMATION: amplification primer
     495 <400> SEQUENCE: 41
E--> 497 gmatgpkppa mggtmtamia gamptmm   ) invalid   27
     512 <210> SEQ ID NO: 43
     513 <211> LENGTH: 27
     514 <212> TYPE: DNA
C--> 515 <213> ORGANISM: Artificial
     517 <220> FEATURE
     518 <223> OTHER INFORMATION: amplification primer
     520 <400> SEQUENCE: 43
E--> 521 gmatgtgmta mggtmtimga gaamtmc   ) invalid   27
     524 <210> SEQ ID NO 44
     525 <211> LENGTH: 27
     526 <212> TYPE: DNA
C--> 527 <213> ORGANISM: Artificial   ← These two error types exist
     52 <220> FEATURE: throughout Sequence Listing
     530 <223> OTHER INFORMATION: amplification primer
     531 <400> SEQUENCE 44   ) invalid ←   27
E--> 533 gmatgtgmta mggtmtimga gakmtmc   27
     1109 <210> SEQ ID NO: 93
     1110 <211> LENGTH: 61
     1111 <212> TYPE: DNA
     1112 <213> ORGANISM HCV
     1114 <400> SEQUENCE 93
E--> 1115 ggtactgcct gatagggtgc ttgcgagtgc cccgggaggt ctcgtagacc   61 50 ← insert cumulative
E--> 1116 gtgcaccatg a   61   base total at
     1119 <210> SEQ ID NO: 94   right margin of
     1120 <211> LENGTH: 61   each line
     1121 <212> TYPE: DNA
     1122 <213> ORGANISM: HGBV-B
     1124 <400> SEQUENCE: 94
E--> 1125 cgtactgcct gatagggtcc ttgcgagggg atctggagt ctcgtagacc   (61) 50
E--> 1126 gtagcacatg c   61 ←

**The types of errors shown exist <u>throughout</u> the Sequence Listing. Please check
<u>all</u> sequences for similar errors.**

VERIFICATION SUMMARY   DATE: 04/30/2001
PATENT APPLICATION: US/09/530,746   TIME: 17:59 39

Input Set : A:\4817 0Q.txt
Output Set: N:\CRF3\04302001\I530746.raw

L:13 M:171 C: Current Application Number differs. Replaced Current Application Number
L:14 M:171 C: Current Filing Date differs. Replaced Current Filing Date
L:23 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:35 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:47 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:59 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:71 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:119 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 10
L:131 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 11
L:143 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 12
L:155 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 13
L:167 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 14
L:179 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 15
L:191 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#.16
L:203 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 17
L:215 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#.18
L:227 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 19
L:239 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 20
L:251 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 21
L:257 M:329 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS.2
L:263 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 22
L:269 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS.1
L:275 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#.23
L:281 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS 2
L:287 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 24
L:293 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS 2
L:299 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#.25
L:305 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS.4
L:311 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 26
L:317 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS 2
L:323 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#.27
L:335 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 28
L:341 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS 2
L:347 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#.29
L:353 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS.1
L:359 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#.30
L:365 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS.2
L:371 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 31
L:377 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS.2
L:383 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 32
L:389 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:395 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#.33
L:407 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 34
L:419 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 35
L:425 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:431 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 36
L:437 M:320 E (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:443 M:220 C Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 37

VERIFICATION SUMMARY   DATE: 04/30/2001
PATENT APPLICATION: US/09/530,746   TIME: 17:59:39

Input Set : A:\4817 0Q.txt
Output Set: N:\CRF3\04302001\I530746.raw

```
L:449 M:320 E:  (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:455 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
L:461 M:320 E:  1  Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:467 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39
L:473 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:479 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40
L:485 M:320 E:  1; Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:491 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41
L:497 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:503 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:515 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43
L:521 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:527 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44
L:543 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:549 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45
L:545 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:551 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 46
L:563 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47
L 569 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L 575 M:220 C. Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 48
L 581 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L 587 M:220 C  Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 49
L 593 M:320 E  (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L 599 M:220 C  Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 50
L 611 M:220 C  Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 51
L 623 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 52
L:635 M:220 C  Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:53
L 647 M:220 C. Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID# 54
L 1115 M:254 E: No. of Bases conflict, LENGTH:Input:61 Counted:50 SEQ:93
M:254 Repeated in SeqNo=93
L:1125 M:254 E: No. of Bases conflict, LENGTH:Input:61 Counted:50 SEQ:94
M:254 Repeated in SeqNo=94
```